

# Package ‘ERSA’

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**Type** Package

**Title** Exploratory Regression 'Shiny' App

**Version** 0.1.0

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**Description** Constructs a 'shiny' app function with interactive displays for summary and analysis of variance regression tables, and parallel coordinate plots of data and residuals.

**License** GPL (>= 2.0)

**Encoding** UTF-8

**LazyData** true

**Imports** shiny, RColorBrewer, ggplot2, car, leaps, broom, dplyr, modelr, tidyr, purrr, combinat, stats, methods

**RoxygenNote** 6.0.1

**Suggests** knitr, rmarkdown

**VignetteBuilder** knitr

**NeedsCompilation** no

**Repository** CRAN

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createERServer	<i>A function which returns a shiny server for Exploratory Regression</i>
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**Description**

A function which returns a shiny server for Exploratory Regression

**Usage**

```
createERServer(ERfit, ERdata = NULL, ERbarcols = RColorBrewer::brewer.pal(4,
  "Set2"), ERnpcpCols = 4, pvalOrder = F)
```

**Arguments**

ERfit	the lm fit to be explored
ERdata	the data used to fit the model. If NULL, attempts to extract from ERfit.
ERbarcols	a vector of colours, one per term in lm. Will be expanded via colorRampPalette if not the correct length.
ERnpcpCols	number of colours for the PCP
pvalOrder	if TRUE, re-arranges predictors in order of p-value

**Value**

a function

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createERUI	<i>Constructs UI for Exploratory Regression app</i>
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**Description**

Constructs UI for Exploratory Regression app

**Usage**

```
createERUI()
```

**Value**

the UI

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ERSA

*ERSA: A package exploring regressions with a Shiny app*

---

### Description

ERSA: A package exploring regressions with a Shiny app

---

exploreReg

*A function to launch the Exploratory Regression Shiny App*

---

### Description

A function to launch the Exploratory Regression Shiny App

### Usage

```
exploreReg(ERmfull, ERdata = NULL, ERbarcols = RColorBrewer::brewer.pal(4,
  "Set2"), npcCols = 4, pvalOrder = F)
```

### Arguments

ERmfull	the lm fit to be explored
ERdata	the data used to fit the model. If NULL, attempts to extract from ERmfull.
ERbarcols	a vector of colours, one per term in lm. Will be expanded via colorRampPalette if not the correct length.
npcCols	number of colours for the PCP
pvalOrder	if TRUE, re-arranges predictors in order of p-value

### Value

the shiny server

### Examples

```
f <- lm(mpg ~ hp+wt+disp, data=mtcars)
## Not run: exploreReg(f)
```

---

 pcpPlot

*A PCP plot of the data, residuals or hat values from regression fits*


---

**Description**

A PCP plot of the data, residuals or hat values from regression fits

**Usage**

```
pcpPlot(data, fit, type = "Variables", npcpCols = 4, resDiff = F,
  absResid = F, sequential = F, selnum = NULL)
```

**Arguments**

data	a data frame
fit	a lm for the data frame
type	one of "Variables", "Residuals", "Hatvalues"
npcpCols	number of colours
resDiff	difference residuals, TRUE or FALSE
absResid	absolute residuals, TRUE or FALSE
sequential	use sequential fits (TRUE) or drop1 fits (FALSE)
selnum	row numbers of cases to be highlighted

**Value**

ggplot

**Examples**

```
f <- lm(mpg ~ wt+hp+disp, data=mtcars)
pcpPlot(mtcars, f, type="Residuals")
```

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 plotSeqSS

*Plots barcharts of sequential sums of squares of lm*


---

**Description**

Plots barcharts of sequential sums of squares of lm

**Usage**

```
plotSeqSS(fits, barcols = NULL, legend = F)
```

**Arguments**

fits	list of lm objects
barcols	a vector of colours, one per term in lms
legend	TRUE or FALSE

**Value**

a ggplot

**Examples**

```
plotSeqSS(list(fit1= lm(mpg ~ wt+hp+disp, data=mtcars),
fit2=lm(mpg ~ wt*hp*disp, data=mtcars)))
```

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plotSum

*Plots of model summaries*


---

**Description**

Plots of model summaries

**Usage**

```
plotAnovaStats(fit0, barcols = NULL, preds = NULL, alpha = 0.05,
type = "SS", width = 0.3)
```

```
plottStats(fit0, barcols = NULL, preds = NULL, alpha = 0.05,
width = 0.3)
```

```
plotCIStats(fit0, barcols = NULL, preds = NULL, alpha = 0.05,
stdunits = FALSE, width = 0.3)
```

**Arguments**

fit0	is an lm object
barcols	a vector of colours, one per term in lm
preds	terms to include in plot
alpha	significance level
type	"SS" or "F", from type 3 Anova
width	bar width
stdunits	TRUE or FALSE. If TRUE, coefficients refer to standardised predictor units.

**Value**

a ggplot

**Functions**

- plotAnovaStats: Plots barchart of F or SS from lm
- plottStats: Plots barchart of t stats from lm
- plotCIStats: Plots confidence intervals from lm

**Examples**

```
plotAnovaStats(lm(mpg ~ wt+hp+disp, data=mtcars))
plottStats(lm(mpg ~ wt+hp+disp, data=mtcars))
plotCIStats(lm(mpg ~ wt+hp+disp, data=mtcars))
```

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reorderTerms	<i>Re-order model terms</i>
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**Description**

Re-order model terms

**Usage**

```
pvalOrder(m, d = NULL, refit = TRUE)
bselOrder(m, d = NULL, refit = TRUE, maxNPred = NULL)
fselOrder(m, d = NULL, refit = TRUE, maxNPred = NULL)
revPredOrd(m, d = NULL, refit = TRUE)
randomPredOrder(m, d = NULL, refit = TRUE)
regsubsetsOrder(m, d = NULL, refit = TRUE, collapse = TRUE)
```

**Arguments**

m	an lm object
d	the data frame. If NULL, attempts to extract from m.
refit	TRUE or FALSE
maxNPred	maximum number of predictors to use, defaults to all.
collapse	TRUE or FALSE

**Value**

a vector of terms in order last to first, or an lm if refit=TRUE. regsubsetsOrder returns a list of predictor vectors, or a list of fits

**Functions**

- pvalOrder: Arranges model terms in order of increasing p-value
- bselOrder: Arranges model terms using backwards selection
- fselOrder: Forwards selection
- revPredOrd: Reverses order of terms in a fit
- randomPredOrder: Reorders terms in a fit randomly
- regsubsetsOrder: Best subsets regression.

**Examples**

```
bse1Order(lm(mpg~wt+hp+disp, data=mtcars))
fse1Order(lm(mpg~wt+hp+disp, data=mtcars))
revPredOrd(lm(mpg~wt+hp+disp, data=mtcars))
randomPredOrder(lm(mpg~wt+hp+disp, data=mtcars))
regsubsetsOrder(lm(mpg~wt+hp+disp, data=mtcars))
```

---

termColours

*Constructs colour vector for model terms*

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**Description**

Constructs colour vector for model terms

**Usage**

```
termColours(f, pal = RColorBrewer::brewer.pal(4, "Set2"))
```

**Arguments**

f                    a model fit with term labels  
pal                  use this palette

**Value**

a vector of colours. Residuals are given a grey color

**Examples**

```
termColours(lm(mpg ~ wt+hp, data=mtcars))
```

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